

SEQUENCE LISTING

<110> Crane, Edmund H. III
Rice, Douglas A.

<120> Maize NPR1 Polynucleotides and Methods
of Use

<130> 1090D2

<150> 60/130,692

<151> 1999-04-23

<150> 09/551,778

<151> 2000-04-18

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2154

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (67)...(1929)

<221> 3'UTR

<222> (1933)...(2154)

<221> 5'UTR

<222> (1)...(66)

<400> 1

gtcgtagtagg tccgggtccg gcacaagtag gggctcgcgt cttgcgcttg gcagttgtgg 60
gaagcc atg gag ccg tcg tcg tcc atc acg ttc gcg tcg tcg tcg tcg 108
Met Glu Pro Ser Ser Ser Ile Thr Phe Ala Ser Ser Ser Ser
1 5 10

tac ctg tcc aac ggc tcg agc ccc tgt tcc gtc gcg ctg ccg ccg cca 156
Tyr Leu Ser Asn Gly Ser Ser Pro Cys Ser Val Ala Leu Pro Pro Pro
15 20 25 30

ggg ccg ccc cag act ccc ccg ttg cct gcc ggc cag ggg tgg ggt ggt 204
Gly Pro Pro Gln Thr Pro Pro Leu Pro Ala Gly Gln Gly Trp Gly Gly
35 40 45

gga gtc gct gcc gca ggg agc gga ggc agc gtg gag gcc gtg agc ctg 252
Gly Val Ala Ala Ala Gly Ser Gly Gly Ser Val Glu Ala Val Ser Leu
50 55 60

aac cgg ctc agc aaa aac ctc gag cgg ctg ctc ctc gac ccg gac cta 300
Asn Arg Leu Ser Lys Asn Leu Glu Arg Leu Leu Leu Asp Pro Asp Leu
65 70 75

gac tgc agc gac gcc gac gtc gat gtg ccc gac ggt ggg ccg ccc gta 348
Asp Cys Ser Asp Ala Asp Val Asp Val Pro Asp Gly Gly Pro Pro Val
80 85 90

FASTA format

ccc atc cac cgc tgc atc ctt gcc gca cgc agc gac ttc ttc tac gac	396
Pro Ile His Arg Cys Ile Leu Ala Ala Arg Ser Asp Phe Phe Tyr Asp	
95 100 105 110	
ctc ttc gcc gct cgc ggc cgc gca ggg gca gcg cgc ggt gat gcg gcc	444
Leu Phe Ala Ala Arg Gly Arg Ala Gly Ala Ala Arg Gly Asp Ala Ala	
115 120 125	
gcc ggc gcc gga gta gcc gcg gag ggg gct gcc agt gga agg ccg cgg	492
Ala Gly Ala Gly Val Ala Ala Glu Gly Ala Ala Ser Gly Arg Pro Arg	
130 135 140	
tac aag atg gag gat ctc gtt ccc gcc ggc cgc gtg ggg cgc gag gcc	540
Tyr Lys Met Glu Asp Leu Val Pro Ala Gly Arg Val Gly Arg Glu Ala	
145 150 155	
ttc cag gcg ttt ctg ggg tac ctg tac acc ggc aag ctc cgg ccg gca	588
Phe Gln Ala Phe Leu Gly Tyr Leu Tyr Thr Gly Lys Leu Arg Pro Ala	
160 165 170	
ccg gtc gac gtg gtg tct tgt gct gac cca gtg tgc cat cac gat tcg	636
Pro Val Asp Val Val Ser Cys Ala Asp Pro Val Cys His His Asp Ser	
175 180 185 190	
tgc ccg ccg gcc atc agg tcc gcg gtc gag ctc atg tac gcg gcg tgt	684
Cys Pro Pro Ala Ile Arg Ser Ala Val Glu Leu Met Tyr Ala Ala Cys	
195 200 205	
acc ttc aag atc ccc gag ctc acc tcg ctc ttc cag cgc cgg ctt ctt	732
Thr Phe Lys Ile Pro Glu Leu Thr Ser Leu Phe Gln Arg Arg Leu Leu	
210 215 220	
aat ttt gta gac aag act cta gtg gag gat gtt att cct att ctg gaa	780
Asn Phe Val Asp Lys Thr Leu Val Glu Asp Val Ile Pro Ile Leu Glu	
225 230 235	
gtt gct tcc cac tca ggg ctg act caa gtg atc gac aaa tgt att caa	828
Val Ala Ser His Ser Gly Leu Thr Gln Val Ile Asp Lys Cys Ile Gln	
240 245 250	
agg att gct aga tca gat ctc gac gat ata tct ttg gat aag gag ctc	876
Arg Ile Ala Arg Ser Asp Leu Asp Asp Ile Ser Leu Asp Lys Glu Leu	
255 260 265 270	
cct cca gaa gca gtt gat gag ata aaa aat ttg cgc aag aag tca caa	924
Pro Pro Glu Ala Val Asp Glu Ile Lys Asn Leu Arg Lys Lys Ser Gln	
275 280 285	
act gct gat ggt gat acg ttc att tcg gac oct gtg cat gag aaa aga	972
Thr Ala Asp Gly Asp Thr Phe Ile Ser Asp Pro Val His Glu Lys Arg	
290 295 300	
gtc aga aga atc cac agg gca ctt gac tct gat gat gtt gag ctt gtg	1020
Val Arg Arg Ile His Arg Ala Leu Asp Ser Asp Asp Val Glu Leu Val	
305 310 315	
aag ttg ctt ctt aat gag tcc gac atc aca tta gat gat gcc aac gca	1068
Lys Leu Leu Leu Asn Glu Ser Asp Ile Thr Leu Asp Asp Ala Asn Ala	
320 325 330	
tta cac tat gct gct tct tac tgt gat cct aaa gtt gtc tca gag ctg	1116
Leu His Tyr Ala Ala Ser Tyr Cys Asp Pro Lys Val Val Ser Glu Leu	

1004759-0150E

335	340	345	350	
tta gat ttg gca atg gct aac tta aat ttg aag aat agc cgt ggg tac				1164
Leu Asp Leu Ala Met Ala Asn Leu Asn Leu Lys Asn Ser Arg Gly Tyr				
	355	360	365	
aca gca ctc cac ttg gct gct atg agg aga gaa cca gct ata atc atg				1212
Thr Ala Leu His Leu Ala Ala Met Arg Arg Glu Pro Ala Ile Ile Met				
	370	375	380	
tgt ctc ctt aac aaa ggg gca aat gtg tca caa ctg aca gct gat ggc				1260
Cys Leu Leu Asn Lys Gly Ala Asn Val Ser Gln Leu Thr Ala Asp Gly				
	385	390	395	
agg agc gca att ggt att tgt cgg agg tta aca aga gca aaa gac tac				1308
Arg Ser Ala Ile Gly Ile Cys Arg Arg Leu Thr Arg Ala Lys Asp Tyr				
	400	405	410	
aat aca aag atg gag cag ggt caa gaa tca aat aaa gat agg ctg tgt				1356
Asn Thr Lys Met Glu Gln Gly Gln Glu Ser Asn Lys Asp Arg Leu Cys				
	415	420	425	430
ata gat att cta gag agg gag atg atg cgg aat cct atg gcg gtg gaa				1404
Ile Asp Ile Leu Glu Arg Glu Met Met Arg Asn Pro Met Ala Val Glu				
	435	440	445	
gat gcc gtc acc tcg cct ttg ttg gca gat gat ctt cac atg aag ctt				1452
Asp Ala Val Thr Ser Pro Leu Leu Ala Asp Asp Leu His Met Lys Leu				
	450	455	460	
ctc tac ctg gaa aac aga gtt gca ttt gct aga ttg ttc ttt cct gct				1500
Leu Tyr Leu Glu Asn Arg Val Ala Phe Ala Arg Leu Phe Phe Pro Ala				
	465	470	475	
gaa gcc aag gtc gcc atg caa atc gca caa gca gac acc aca gaa gaa				1548
Glu Ala Lys Val Ala Met Gln Ile Ala Gln Ala Asp Thr Thr Glu Glu				
	480	485	490	
ttc ggc ggt ata gtt gca gtt gca gca agc act tct ggt aaa ctg agg				1596
Phe Gly Gly Ile Val Ala Val Ala Ala Ser Thr Ser Gly Lys Leu Arg				
	495	500	505	510
gag gtg gac ctt aat gag acg cca gtg aca caa aac aaa agg ctc cgt				1644
Glu Val Asp Leu Asn Glu Thr Pro Val Thr Gln Asn Lys Arg Leu Arg				
	515	520	525	
tca agg gta gat gca ctg atg aaa aca gtg gag ctg ggc cgt cgg tac				1692
Ser Arg Val Asp Ala Leu Met Lys Thr Val Glu Leu Gly Arg Arg Tyr				
	530	535	540	
ttc ccg aac tgc tcg cag gtg ctg gac aag ttc ctg gag gac gat ctg				1740
Phe Pro Asn Cys Ser Gln Val Leu Asp Lys Phe Leu Glu Asp Asp Leu				
	545	550	555	
ccg gaa ggt ctg gac cag ttc tac ctc cag agg ggc aca gcc gat gag				1788
Pro Glu Gly Leu Asp Gln Phe Tyr Leu Gln Arg Gly Thr Ala Asp Glu				
	560	565	570	
cag aag gtg aag agg atg cgc ttc tgc gag ctg aaa gag gac gtg ctg				1836
Gln Lys Val Lys Arg Met Arg Phe Cys Glu Leu Lys Glu Asp Val Leu				
	575	580	585	590

1004499
E6544007

aag gcg ttt agc aag gac aag gcg gag ggc agc gtg ttc tcg ggc ctg 1884
 Lys Ala Phe Ser Lys Asp Lys Ala Glu Gly Ser Val Phe Ser Gly Leu
 595 600 605

tcc tcg tcg tcg tcg tgc tcg ccg ccc cag aag tat gcc cag agg 1929
 Ser Ser Ser Ser Ser Cys Ser Pro Pro Gln Lys Tyr Ala Gln Arg
 610 615 620

tgatcaaggc accagttttt gccgtatagt ttgttatcat ggtcttcgag acttggaccc 1989
 ggacagcata tagggacatg tacacctgtg tatgtatagt gcttacaatt gccgtaagta 2049
 gaactatatg tatggaacat aaggaaacat ggcaggaaca ccgtgcaaaa agatgaaaag 2109
 atggccgaag tgctctatgc gaaaaaaaaa aaaaaaaaaa aaaaa 2154

<210> 2
 <211> 621
 <212> PRT
 <213> Zea mays

<400> 2
 Met Glu Pro Ser Ser Ser Ile Thr Phe Ala Ser Ser Ser Ser Tyr Leu
 1 5 10 15
 Ser Asn Gly Ser Ser Pro Cys Ser Val Ala Leu Pro Pro Pro Gly Pro
 20 25 30
 Pro Gln Thr Pro Pro Leu Pro Ala Gly Gln Gly Trp Gly Gly Gly Val
 35 40 45
 Ala Ala Ala Gly Ser Gly Gly Ser Val Glu Ala Val Ser Leu Asn Arg
 50 55 60
 Leu Ser Lys Asn Leu Glu Arg Leu Leu Leu Asp Pro Asp Leu Asp Cys
 65 70 75 80
 Ser Asp Ala Asp Val Asp Val Pro Asp Gly Gly Pro Pro Val Pro Ile
 85 90 95
 His Arg Cys Ile Leu Ala Ala Arg Ser Asp Phe Phe Tyr Asp Leu Phe
 100 105 110
 Ala Ala Arg Gly Arg Ala Gly Ala Ala Arg Gly Asp Ala Ala Ala Gly
 115 120 125
 Ala Gly Val Ala Ala Glu Gly Ala Ala Ser Gly Arg Pro Arg Tyr Lys
 130 135 140
 Met Glu Asp Leu Val Pro Ala Gly Arg Val Gly Arg Glu Ala Phe Gln
 145 150 155 160
 Ala Phe Leu Gly Tyr Leu Tyr Thr Gly Lys Leu Arg Pro Ala Pro Val
 165 170 175
 Asp Val Val Ser Cys Ala Asp Pro Val Cys His His Asp Ser Cys Pro
 180 185 190
 Pro Ala Ile Arg Ser Ala Val Glu Leu Met Tyr Ala Ala Cys Thr Phe
 195 200 205
 Lys Ile Pro Glu Leu Thr Ser Leu Phe Gln Arg Arg Leu Leu Asn Phe
 210 215 220
 Val Asp Lys Thr Leu Val Glu Asp Val Ile Pro Ile Leu Glu Val Ala
 225 230 235 240
 Ser His Ser Gly Leu Thr Gln Val Ile Asp Lys Cys Ile Gln Arg Ile
 245 250 255
 Ala Arg Ser Asp Leu Asp Asp Ile Ser Leu Asp Lys Glu Leu Pro Pro
 260 265 270
 Glu Ala Val Asp Glu Ile Lys Asn Leu Arg Lys Lys Ser Gln Thr Ala
 275 280 285
 Asp Gly Asp Thr Phe Ile Ser Asp Pro Val His Glu Lys Arg Val Arg
 290 295 300
 Arg Ile His Arg Ala Leu Asp Ser Asp Asp Val Glu Leu Val Lys Leu
 305 310 315 320
 Leu Leu Asn Glu Ser Asp Ile Thr Leu Asp Asp Ala Asn Ala Leu His
 325 330 335
 Tyr Ala Ala Ser Tyr Cys Asp Pro Lys Val Val Ser Glu Leu Leu Asp

```

          340          345          350
Leu Ala Met Ala Asn Leu Asn Leu Lys Asn Ser Arg Gly Tyr Thr Ala
          355          360          365
Leu His Leu Ala Ala Met Arg Arg Glu Pro Ala Ile Ile Met Cys Leu
          370          375          380
Leu Asn Lys Gly Ala Asn Val Ser Gln Leu Thr Ala Asp Gly Arg Ser
385          390          395          400
Ala Ile Gly Ile Cys Arg Arg Leu Thr Arg Ala Lys Asp Tyr Asn Thr
          405          410          415
Lys Met Glu Gln Gly Gln Glu Ser Asn Lys Asp Arg Leu Cys Ile Asp
          420          425          430
Ile Leu Glu Arg Glu Met Met Arg Asn Pro Met Ala Val Glu Asp Ala
          435          440          445
Val Thr Ser Pro Leu Leu Ala Asp Asp Leu His Met Lys Leu Leu Tyr
          450          455          460
Leu Glu Asn Arg Val Ala Phe Ala Arg Leu Phe Phe Pro Ala Glu Ala
465          470          475          480
Lys Val Ala Met Gln Ile Ala Gln Ala Asp Thr Thr Glu Glu Phe Gly
          485          490          495
Gly Ile Val Ala Val Ala Ala Ser Thr Ser Gly Lys Leu Arg Glu Val
          500          505          510
Asp Leu Asn Glu Thr Pro Val Thr Gln Asn Lys Arg Leu Arg Ser Arg
          515          520          525
Val Asp Ala Leu Met Lys Thr Val Glu Leu Gly Arg Arg Tyr Phe Pro
          530          535          540
Asn Cys Ser Gln Val Leu Asp Lys Phe Leu Glu Asp Asp Leu Pro Glu
545          550          555          560
Gly Leu Asp Gln Phe Tyr Leu Gln Arg Gly Thr Ala Asp Glu Gln Lys
          565          570          575
Val Lys Arg Met Arg Phe Cys Glu Leu Lys Glu Asp Val Leu Lys Ala
          580          585          590
Phe Ser Lys Asp Lys Ala Glu Gly Ser Val Phe Ser Gly Leu Ser Ser
          595          600          605
Ser Ser Ser Cys Ser Pro Pro Gln Lys Tyr Ala Gln Arg
          610          615          620

```

```

<210> 3
<211> 7789
<212> DNA
<213> Zea mays

<220>
<221> promoter
<222> (1)...(2715)

<221> 5'UTR
<222> (2716)...(2781)

<221> exon
<222> (2782)...(3435)

<221> intron
<222> (3436)...(3987)

<221> exon
<222> (3988)...(4738)

<221> intron
<222> (4739)...(5274)

<221> exon

```

20570" E6524001

<222> (5275) ... (5475)

<221> intron

<222> (5476) ... (5665)

<221> exon

<222> (5666) ... (5922)

<221> 3'UTR

<222> (5926) ... (6124)

<400> 3

gcggccgcgt	aatacgactc	actatagggc	gaagaattcg	gatctccttc	cttattttggc	60
gaagccgacc	gttggcgctt	tggagccggt	ggcgacccgg	acactgtccg	gtgcacaccg	120
gacagtcagg	tgcctccctc	cgaccgttgg	ctcggccaag	tgcttcgcgc	ggatcgcgcg	180
gcagaccgtt	ggcccgaccg	accgttgggt	caccggacag	tccggtgcac	accagacagt	240
ccggtgaatt	atagccgtac	gccgttaatc	acttcccag	agcagcaagt	tcgcctgagc	300
cagcctggcg	caccggacac	tgtccggtga	accacccggc	agtcgggtgc	acccagtacg	360
agctgacttt	ggctgaacaa	agtcactctt	agttccaact	tgatttttcc	tgtttccagc	420
acttagacac	aatacattag	tctctaaaac	aatgtattaa	ttctgagaaa	cataccttta	480
tacttggttt	gtactttgtc	caccatttaa	cacttgggca	cttgtgttgg	acactaaatc	540
acaaaaatac	ttagaaatgg	cccaagggca	catttccctt	tcaacagtc	ggtgccacac	600
cggacagtcc	ggtgacctct	gacttctgtg	ttctaacttc	tgtcgcggca	ctgtttcgca	660
ctatagcggt	ttgcagtcga	ccgttggcgc	acagagagcc	attgctccgc	tggctgaccg	720
gacagtcoga	tgaattatag	cggascgcgc	ctctgaattc	ccgagtgtgg	cctgtttgaa	780
gggcgcctgg	cctggtgcac	cgaacaatgt	atgggtgcgc	aaaaatcagc	acactcaagt	840
cctttgcttc	attttttatt	gtgtcgctaa	ctggatttct	ttttggtttg	tggtgaacct	900
tatgcacctg	agataaatca	catctagcca	aactagttag	tccatgtggg	ttgtgttgat	960
cgtcaactac	taaaatctat	ttatagaaag	tggttaaccc	tatttccctt	tcagcacact	1020
ctatatagtg	cttgagacct	cgacatgaag	gtgtcctagg	aagccaaggc	tctcgcgtaa	1080
ggtcctcgac	atgcaggacc	ctagggcccg	ttagaatggg	gcttgtccat	aagagagttg	1140
ggctctaaga	tgcattgactg	acactgtgcg	tctgtcggtt	cttaataaag	ttatagatga	1200
tgttttgcca	acatctgatg	atatgtcttg	gtgcttacaa	aagccttggt	ttttatcttc	1260
ctttcgtctt	aataaagatc	catattacat	ttatatattac	tatgtcatat	atatacctca	1320
ctatctcgaa	gatacatctc	gttgcggaag	cataaggtag	ctttggaggt	aaagcttaga	1380
gcgacatgtg	ggtgcaacaa	acaaacatgg	gggcacaaca	cacctcacct	catataacta	1440
atttggcttg	caaatcgaga	gtcccgtacg	aaaagtactc	gttgtctctt	gacccaataa	1500
atcaaataca	ccttcttaca	caatttgtcc	attttatatt	tttcgtttcc	aataacaaac	1560
tcaaagtgc	ttgttttttt	ggacctttga	cacatagcct	ttaaagtaga	tttcacaatt	1620
taagcttggt	atgtaaaaca	aactaatttc	gagagaggct	gattgaggag	aaagtctcgc	1680
gtcgatgatt	caattggacg	aaatcgatgt	ttaaactgtc	ttgttgatta	aatttctagc	1740
ttcacacgtg	cttgaacggc	gtaggaagtg	ttggaatttc	ccttcttatg	atattattaga	1800
gtagagtttt	gttacagttt	atttacggat	tcattacggg	atttattagg	gatacgttga	1860
catataactt	cagtctttct	tttttaatat	tcacaagaaa	ctttcacaca	cctactagga	1920
gtaacagaaa	aacatggaca	tattgatttt	tgaaaaaaga	aatattgaca	gataaggtgt	1980
tggggaccgt	agagactaga	gaggatgagg	acgacgccag	gcagacgagc	cttgccgatt	2040
gccgtcgacg	tcaccctggg	caggcgctcac	ttgacgacgt	atacaggggc	acagggctca	2100
ggttttccct	caaattgcgc	cgaaatactc	gagatttctt	ggattttttt	acttgtttat	2160
tctattctcc	ttccggcgcc	tctctagtct	attctccttc	ctcgtcgagt	cgtcgtcttc	2220
ttcgatccac	tctttccccc	atccctatct	ccctactttc	cacgcaactg	cgtttccccc	2280
ggactcttct	tccacgatcc	cgttggaccc	ctaccgctcc	tcagtcagtc	ctcgcctctc	2340
ccagcaccgg	ccaacaatcc	ctcacgttat	tcctgttagc	tactatgctg	ccctcttgga	2400
tccctttttc	acttgtctga	gatttagcca	ccgcccggta	ggaagaagaa	ggggaagcac	2460
catattttct	gttccctggc	tgacgcagcg	ccggtgagat	ttcagtcagg	gatcggcaac	2520
gctgggagga	ctcgcgtgtg	atttacgccg	acttccgtgc	cgctctagga	agggtcacgt	2580
cgaggaggct	ttgtccgacg	cggatttgcc	tggagccagc	caagcagagc	gcagaattgg	2640
gggtgttttg	cctgtcgaag	ccagaaaagt	ctcggtttgg	ctgccgaaac	cgttgaggc	2700
gaccaccatc	tcattggtcgt	agtgttcggg	gtccggcaca	agtaggggct	cgcgtcttgc	2760
gcttggcagt	tgtgggaagc	catggagccg	tcgtcgtcca	tcacgttcgc	gtcgtcgtcg	2820
tcgtacctgt	ccaacggctc	gagccctgt	tcogtcgcgc	tgccgcgcgc	agggccgccc	2880
cagactcccc	cgttgccctgc	cggccagggg	tggggtgggtg	gagtcgctgc	cgcaggagagc	2940
ggaggcagcg	tggaggccgt	gagcctgaac	cggctcagca	aaaacctcga	gcggctgctc	3000

ctcgacccgg	acctagactg	cagcgacgcc	gacgtcgatg	tgcccgaagg	tgggcccggc	3060
gtacccatcc	accgctgcat	ccttgccgca	cgcagcgact	tcttctacga	cctcttcgcc	3120
gctcgcggcc	gcgcaggggc	agcgcgcggg	gatgcggccg	ccggcgccgg	agtagccggc	3180
gagggggctg	ccagtgggaag	gccgcggtag	aagatggagg	atctcgttcc	cgccggccgc	3240
gtggggcgcg	aggccttcca	ggcgtttctg	gggtacctgt	acaccggcaa	gctccggccg	3300
gcaccggctg	acgtgggtgc	ttgtgctgac	ccagtgtgcc	atcacgattc	gtgcccgcgc	3360
gccatcaggt	ccgcggtcga	gctcatgtac	gcggcggtga	ccttcaagat	ccccgagctc	3420
acctcgctct	tccaggtgag	acgcaatttg	gttcttgctc	gccccattgt	caataggatt	3480
aaactcta	ttcttttagga	attgtttcgt	tctatgccaa	tactgtacat	ggcttcggta	3540
gactagaaat	ggatttgtga	ttttttttct	ccaatccgag	tgttgactac	atcactacaa	3600
aaagctatca	atagctgaac	tgctaaaatt	gctgattttg	ttttctccaa	tccgagtgtt	3660
gaccacatca	ctgcaaaaag	ttattaatag	ctgaatcgct	acaattgttc	aattgttgat	3720
tttggttttt	ccaatccgag	tggtgacact	acaaaaaact	attaatagt	gaactactaa	3780
aattgtttgg	tattgctttt	ttagtgtgatt	caagcgaaac	tggtggcttg	aagtctatga	3840
attgaaatgg	aatcattatt	cattaggctg	ctcaacattt	gtatattaca	tttatggctg	3900
tataattttat	caatctgttt	aacatcaatt	cagctttgct	ttgtcgattt	atggaaggca	3960
aatgggttaac	atgggtctct	tctacagcgc	cggcttctta	attttgtaga	caagactcta	4020
gtggaggatg	ttattcctat	tctggaagtt	gcttcccact	cagggctgac	tcaagtgatc	4080
gacaaatgta	ttcaaaggat	tgctagatca	gatctcgacg	atatactctt	ggataaggag	4140
ctccctccag	aagcagttga	tgagataaaa	aatttgcgca	agaagtcaca	aactgctgat	4200
ggtgatacgt	tcatttcgga	ccctgtgcat	gagaaaagag	tcagaagaat	ccacagggca	4260
cttgactctg	atgatgttga	gcttgtggaag	ttgcttctta	atgagtcgga	catcacatta	4320
gatgatgcca	acgcattaca	ctatgctgct	tcttactgtg	atcctaaaagt	tgtctcagag	4380
ctggttagatt	tggaatggc	taacttaaat	ttgaagaata	gccgtgggta	cacagcactc	4440
cacttggtcg	ctatgaggag	agaaccagct	ataatcatgt	gtctccttaa	caaaggggca	4500
aatgtgtcac	aactgacagc	tgatggcagg	agcgcaattg	gtatttgtcg	gaggttaaca	4560
agagcaaaaag	actacaatac	aaagatggag	caggggtcaag	aatcaaataa	agataggctg	4620
tgtatagata	ttctagagag	ggagatgatg	cggaatccta	tggcggtgga	agatgccgtc	4680
acctcgctct	tgttggcaga	tgatcttcac	atgaagcttc	tctacctgga	aaacagaggt	4740
gaagtcacata	ccatgcttga	tagaatggct	ctgattgggt	gcctgttgcc	gcttcaaatt	4800
ttgaaaattt	aaaagcttgg	aggtcagggtg	gattgattca	ggctagcttg	tagactaatg	4860
acatgtgcct	gaccttttgt	tctcataaag	agggaaaaag	gaaaaacgcc	acccataacc	4920
acatcaattt	ctcctttttt	tcaaattggg	gaaagctgta	catgttgtag	gaaataaaca	4980
attgtagtca	caaagcccaa	attaatctaa	ttacagatga	caagcctgga	ttattaaatt	5040
gccacttgcc	tgtccatatt	gcacacaacc	tagtagtgct	ctagttctag	ataatataac	5100
gagaatgatt	tcacaccact	ggatgatgat	caaatagcac	cttagaactt	ggggttgagg	5160
tatgtcattg	tcgtgagctt	tgtcttatgt	tcacgtttat	aagaagattg	tgatttatgt	5220
tattggctac	attattttcc	ctgcaccata	acattctaa	tattgttcc	gcagttgcat	5280
ttgctagatt	gttcttttcc	gctgaagcca	aggtcgccat	gcaaactcgca	caagcagaca	5340
ccacagaaga	attcggcggt	atagttgcag	ttgcagcaag	cacttctggt	aaactgagg	5400
aggtggacct	taatgagacg	ccagtgcac	aaaacaaaag	gctccgttca	agggttagatg	5460
cactgatgaa	aacaggtgaa	agtttcaacc	gtcaaccttt	tccattgtag	tgaacatgcc	5520
ctgcagctat	ctccagaaaa	tttagttcgg	acgcaatcac	ggattctacg	tgtacctgaa	5580
gtattgtgac	tatgttcaaa	atacatgatt	gatacaatgt	atctgatctg	gtgttcgccc	5640
atttttatcc	gatgacttct	tgcaaggag	ctgggcccgtc	ggtacttccc	gaactgctcg	5700
caggtgctgg	acaagttcct	ggaggacgat	ctgccggaag	gtctggacca	gttctacctc	5760
cagaggggca	cagccgatga	gcagaagggtg	aagaggatgc	gcttctgcga	gctgaaagag	5820
gacgtgctga	aggcgtttag	caaggacaag	gcggagggca	gcgtgttctc	gggcctgtcc	5880
tcgtcgctcg	cgtgctcgcc	gccccagaag	atgcccaga	ggtgatcaag	gcaccagt	5940
ttgccgtata	gtttgtttatc	atggctcttcg	agacttgga	ccggacagca	tatagggaca	6000
tgtacacctg	tgtatgtata	gtgcttacia	ttggcgtaag	tagaactata	tgtatggaac	6060
ataaggaaac	atggcaggaa	caccgtgcaa	aaagatgaaa	agatggccga	agtgtcttat	6120
gcgagtgccc	acctgattcg	atggccctat	tcaacggcgc	cctgtcagca	tgctgcatgc	6180
ccactgagac	cttcggttgc	atagggatag	gaggagattt	ctgttcaatt	ttggctagca	6240
agtgatatag	gggtgttttag	gactgtttca	ctttatgaaa	atcaacttag	ctcataaaca	6300
cttttaactt	caataactta	ggctctgttt	ggagtggctg	tatttttcta	gtcccaagaa	6360
aataatgtgg	tatctgagaa	taccatgggtc	tagaaaccaa	aatgtgtttg	gcagactctt	6420
ttaaaccatg	gtatttataa	tcttgggttt	gacaagacca	cattatttct	gggtatagaa	6480
tactgtccag	actagggtcg	gaaatgagcc	gagttcggct	cggctcggtg	cggctcggtg	6540
actgaacgag	ctcgactcgg	ctcgccatt	ccacgagctg	gtgaaagagg	ctcggtcgg	6600
ctcgacctta	gctcgcgagc	catattcttg	taottatcgt	ttcattattt	gatgaattaa	6660
cattatataa	atgtgaaata	taaaatcatc	attctacatt	atgagtaaat	taaactataa	6720

```

cttgtaatat attcatcatc aaagactaaa aaataagcta ttatccataa aattatctaa 6780
tattttattat tattccataa attgatcatt tttgcaaggc tcgtgagctg gaacgagccg 6840
gctcggctcg gctcgtcgca aaaacgagct cgaagaaggg gctcggcttg gctcgttcga 6900
ggctcgcgag ctgcgcgcgag ccgagccgct ccgagctcga gccggctcgc gagcctcgag 6960
ctaattttcc agccctagtc cagaccaaag tttttcgtca gagcgcgcgga agcgacccta 7020
atgtccgcgc cctttttctca ccgtccacgc atctcttccc ctcaattcta aggttttctc 7080
caacaagaaa cgttaaagcg ttcggtacgc tatatttagc gtgtaccttc gtctccaaca 7140
agcacatgta tagcgttcgc taaaatttag cggagcctca gcgtccgcca aatctagcat 7200
ctcctgtccg tccgctattc tgtcagctct cgtacgggaa gccgtatgct actatcatag 7260
cgccaataaa aaacaaacaa tgccaggaac gtctccgctg accagtaaaa aagaactaaa 7320
aatggaacta aaagatcttc tatggacata tgtgagaacg accatttcat atattcaaca 7380
tcttttagct gtacataaat attttactat gtattctaca ataatttgta atttgttgaa 7440
aaatatgatt gcaataaatt atgttaatat ggttgccaaa atatatacga tgagatatag 7500
aacaacatt gtagtttatg gattatgtta aactgtaga tatagagatt cgaatttagg 7560
tgacgttgct gaagatgaag aagatataga gaacataatc ttttagagaa tgctgtaaag 7620
gacagagaat atttcttttag agaacggaat ttagggtagc ttgctggaga cagcctaata 7680
cagacactct tttcctcttt ctccattccc catcgcaaaa ctgggaggac ctagcttcgc 7740
cgcagatgtc gtcggtcccg ggacgctgat ctgcctcag attcctggtg 7789

```

<210> 4
 <211> 621
 <212> PRT
 <213> Zea mays

<400> 4

Met	Glu	Pro	Ser	Ser	Ser	Ile	Thr	Phe	Ala	Ser	Ser	Ser	Ser	Tyr	Leu
1				5				10						15	
Ser	Asn	Gly	Ser	Ser	Pro	Cys	Ser	Val	Ala	Leu	Pro	Pro	Pro	Gly	Pro
		20						25					30		
Pro	Gln	Thr	Pro	Pro	Leu	Pro	Ala	Gly	Gln	Gly	Trp	Gly	Gly	Gly	Val
		35					40					45			
Ala	Ala	Ala	Gly	Ser	Gly	Gly	Ser	Val	Glu	Ala	Val	Ser	Leu	Asn	Arg
		50				55					60				
Leu	Ser	Lys	Asn	Leu	Glu	Arg	Leu	Leu	Leu	Asp	Pro	Asp	Leu	Asp	Cys
65					70					75				80	
Ser	Asp	Ala	Asp	Val	Asp	Val	Pro	Asp	Gly	Gly	Pro	Pro	Val	Pro	Ile
			85						90					95	
His	Arg	Cys	Ile	Leu	Ala	Ala	Arg	Ser	Asp	Phe	Phe	Tyr	Asp	Leu	Phe
			100					105					110		
Ala	Ala	Arg	Gly	Arg	Ala	Gly	Ala	Ala	Arg	Gly	Asp	Ala	Ala	Ala	Gly
		115				120					125				
Ala	Gly	Val	Ala	Ala	Glu	Gly	Ala	Ala	Ser	Gly	Arg	Pro	Arg	Tyr	Lys
		130				135					140				
Met	Glu	Asp	Leu	Val	Pro	Ala	Gly	Arg	Val	Gly	Arg	Glu	Ala	Phe	Gln
145					150					155				160	
Ala	Phe	Leu	Gly	Tyr	Leu	Tyr	Thr	Gly	Lys	Leu	Arg	Pro	Ala	Pro	Val
			165					170						175	
Asp	Val	Val	Ser	Cys	Ala	Asp	Pro	Val	Cys	His	His	Asp	Ser	Cys	Pro
			180					185					190		
Pro	Ala	Ile	Arg	Ser	Ala	Val	Glu	Leu	Met	Tyr	Ala	Ala	Cys	Thr	Phe
		195				200						205			
Lys	Ile	Pro	Glu	Leu	Thr	Ser	Leu	Phe	Gln	Arg	Arg	Leu	Leu	Asn	Phe
	210					215					220				
Val	Asp	Lys	Thr	Leu	Val	Glu	Asp	Val	Ile	Pro	Ile	Leu	Glu	Val	Ala
225					230					235				240	
Ser	His	Ser	Gly	Leu	Thr	Gln	Val	Ile	Asp	Lys	Cys	Ile	Gln	Arg	Ile
			245					250					255		
Ala	Arg	Ser	Asp	Leu	Asp	Asp	Ile	Ser	Leu	Asp	Lys	Glu	Leu	Pro	Pro
			260				265						270		
Glu	Ala	Val	Asp	Glu	Ile	Lys	Asn	Leu	Arg	Lys	Lys	Ser	Gln	Thr	Ala

205T0"663400T

275 280 285
 Asp Gly Asp Thr Phe Ile Ser Asp Pro Val His Glu Lys Arg Val Arg
 290 295 300
 Arg Ile His Arg Ala Leu Asp Ser Asp Val Glu Leu Val Lys Leu
 305 310 315 320
 Leu Leu Asn Glu Ser Asp Ile Thr Leu Asp Asp Ala Asn Ala Leu His
 325 330 335
 Tyr Ala Ala Ser Tyr Cys Asp Pro Lys Val Val Ser Glu Leu Leu Asp
 340 345 350
 Leu Ala Met Ala Asn Leu Asn Leu Lys Asn Ser Arg Gly Tyr Thr Ala
 355 360 365
 Leu His Leu Ala Ala Met Arg Arg Glu Pro Ala Ile Ile Met Cys Leu
 370 375 380
 Leu Asn Lys Gly Ala Asn Val Ser Gln Leu Thr Ala Asp Gly Arg Ser
 385 390 395 400
 Ala Ile Gly Ile Cys Arg Arg Leu Thr Arg Ala Lys Asp Tyr Asn Thr
 405 410 415
 Lys Met Glu Gln Gly Gln Glu Ser Asn Lys Asp Arg Leu Cys Ile Asp
 420 425 430
 Ile Leu Glu Arg Glu Met Met Arg Asn Pro Met Ala Val Glu Asp Ala
 435 440 445
 Val Thr Ser Pro Leu Leu Ala Asp Asp Leu His Met Lys Leu Leu Tyr
 450 455 460
 Leu Glu Asn Arg Val Ala Phe Ala Arg Leu Phe Phe Pro Ala Glu Ala
 465 470 475 480
 Lys Val Ala Met Gln Ile Ala Gln Ala Asp Thr Thr Glu Glu Phe Gly
 485 490 495
 Gly Ile Val Ala Val Ala Ala Ser Thr Ser Gly Lys Leu Arg Glu Val
 500 505 510
 Asp Leu Asn Glu Thr Pro Val Thr Gln Asn Lys Arg Leu Arg Ser Arg
 515 520 525
 Val Asp Ala Leu Met Lys Thr Val Glu Leu Gly Arg Arg Tyr Phe Pro
 530 535 540
 Asn Cys Ser Gln Val Leu Asp Lys Phe Leu Glu Asp Asp Leu Pro Glu
 545 550 555 560
 Gly Leu Asp Gln Phe Tyr Leu Gln Arg Gly Thr Ala Asp Glu Gln Lys
 565 570 575
 Val Lys Arg Met Arg Phe Cys Glu Leu Lys Glu Asp Val Leu Lys Ala
 580 585 590
 Phe Ser Lys Asp Lys Ala Glu Gly Ser Val Phe Ser Gly Leu Ser Ser
 595 600 605
 Ser Ser Ser Cys Ser Pro Pro Gln Lys Tyr Ala Gln Arg
 610 615 620

<210> 5

<211> 2715

<212> DNA

<213> Zea mays

<220>

<221> promoter

<222> (1)... (2715)

<400> 5

gcggccgcgt	aatacgactc	actatagggc	gaagaattcg	gatctccttc	cttatttggt	60
gaagccgacc	gttggcgctt	tggagccgtt	ggcgcaccgg	acactgtccg	gtgcacaccg	120
gacagtcagg	tgcccccttc	cgaccgttgg	ctcggccacg	tgtttcgcgc	ggatcgcgcg	180
gcagaccgtt	ggcccagacc	accgttggct	caccggacag	tccgggtgcac	accagacagt	240
cgggtgaatt	atagccgtac	gccgttaatc	acttcccag	agcagcaagt	tcgcctgagc	300
cagcctggcg	caccggacac	tgctcgggtg	accaccggac	agtcgggtgc	acccagtcag	360
agctgacttt	ggctgaacaa	agtcactctt	agttccaact	tgatttttcc	tgtttccagc	420

acttagacac	aatacattag	tctctaaaac	aatgtattaa	ttctgagaaa	cataccttta	480
tacttggttt	gtactttgtc	caccatttaa	cacttgggca	cttgtgttgg	acactaaatc	540
acaaaaatac	ttagaaatgg	cccaagggca	catttccctt	tcaacagtcc	ggtgccacac	600
cggacagtcc	ggtgacctct	gacttctgtg	ttctaacttc	tgctcgcgca	ctgtttcgca	660
ctatagcgtt	ttgcagtcga	ccgttggcgc	acagagagcc	attgctccgc	tggctgaccg	720
gacagtcgga	tgaattatag	cggascgcgc	ctctgaattc	ccgagtgtgg	cctgtttgaa	780
ggggcgctgg	cctgggtgcac	cgaacaatgt	atgggtgcgc	aaaaatcagc	acactcaagt	840
ccttttgcttc	attttttatt	gtgtcgctaa	ctggatttct	ttttggtttg	tggtgaacct	900
tatgcacctg	agataaatca	catctagcca	aactagttag	tccatgtggg	ttgtgttgat	960
cgtcaactac	taaaatctat	ttatagaaag	tggttaaccc	tatttccctt	tcagcacact	1020
ctatatagtg	cttgagacct	cgacatgaag	gtgtcctagg	aagccaaggc	tctcgcgtaa	1080
ggtcctcgac	atgcaggacc	ctaggccccg	ttagaatggg	gcttgtccat	aagagagttg	1140
ggctctaaga	tgcagtactg	acactgtgcg	tctgtcgttt	cttaataaag	ttatagatga	1200
tgttttgcca	acatctgatg	atatgtcttg	gtgcttacaa	aagccttggt	ttttatcttc	1260
ctttcgtctt	aataaagatc	catattacat	ttatatttac	tatgtcatat	atatacctca	1320
ctatctcgaa	gatacatctc	gttgcggaag	cataaggtag	ccttgagggt	aaagcttaga	1380
gcgacatgtg	ggtgcaacaa	acaaacatgg	gggcacaaca	cacctcacct	catataacta	1440
atlttggttg	caaactcgaga	gtcccgtagc	aaaagtactc	gttgtctctt	gacccaataa	1500
atcaaatata	ccttcttaca	caatttgtcc	attttatatt	tttcgtttcc	aataacaaac	1560
tcaaagtgac	ttgttttttt	ggacctttga	cacatagcct	ttaaagtaga	tttcacaatt	1620
taagcttggt	atgtaaaaca	aactaatctc	gagagaggct	gattgaggag	aaagtctgcg	1680
gtcgatgatt	caattggacg	aaatcgatgt	ttaaactgtc	ttgttgatta	aatttctagc	1740
ttcacacgtg	cttgaacggc	gtaggaagtg	ttggaatttc	ccttcttatg	atttattaga	1800
gtagagtttt	gttacagttt	atttacggat	tcattacggt	atttattagg	gatacgttga	1860
catataactt	cagtctttct	tttttaatag	tcacaagaaa	ccttcacaca	cctactagga	1920
gtaacagaaa	aacatggaca	tattgatttt	tgaaaaaaga	aatattgaca	gataagggtg	1980
tggggaccgt	agagactaga	gaggatgagg	acgacgccag	gcagacgagc	cttgccgatt	2040
gccgtcgacg	tcaccctggg	caggcgtcac	ttgacgacgt	atacaggggc	acagggctca	2100
ggttttcctt	caaattgcgc	cgaataactc	gagatttctt	ggattttttt	acttggttat	2160
tctattctcc	ttccggcgcc	tctctagtct	attctccttc	ctcgctcgagt	cgctcgtctc	2220
ttcgatccac	tctttccccc	atccctatct	ccctactttc	cacgcaactg	cgtttccccc	2280
ggactcttct	tccacgatcc	cgttggaccc	ctaccgctcc	tcagtcagtc	ctcgccccctc	2340
ccagcaccgg	ccaacaatcc	ctcacgttat	tccctgtagc	tactatgctg	ccctcttgga	2400
tccctttttc	acttgtctga	gatttagcca	ccgcccggtg	ggaagaagaa	ggggaagcac	2460
catattttct	gttcctggcc	tgacgcagcg	ccggtgagat	ttcagtcagg	gatcggaac	2520
gctgggagga	ctcgcggtgtg	atttacgcgc	acttccgtgc	cgctctagga	agggtcacgt	2580
cgaggaggct	tttgccgacg	cggattttgc	tggagccagc	caagcagagc	gcagaattgg	2640
gggtgtttgg	ccgtgcaaag	ccagaaagtt	ctcggtttgg	ctgccgaaac	cgtttgagggc	2700
gaccaccatc	tcattg					2715

<210> 6

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide based upon an adaptor used for cDNA library construction and poly(dT) to remove clones which have a poly(A) tail but no cDNA insert.

<400> 6

tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa

36